

5. Genomic analysis of *Acinetobacter baumannii* prophages reveals remarkable diversity and suggests significant impact on bacterial virulence and fitness

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Bacterial genomics has revealed substantial amounts of prophage DNA in bacterial genomes. This integrated viral DNA has been shown to play important roles in the evolution of bacterial pathogenicity. *Acinetobacter baumannii* has shown a fast progression as a nosocomial multi-resistant pathogen in recent years, and is now considered one of the most dangerous microorganisms in hospital environments. The role of prophages in the evolution of *A. baumannii* pathogenicity has not yet been explored. In this context, we aimed at evaluating the impact of prophages on *A. baumannii* genomic diversity and pathogenicity.

Approximately 959 strains were analyzed for the presence of intact and defective prophages using PHAST. A total of 6691 prophages were detected, with all strains having at least one prophage and 83.4% encoding intact prophages. A subset of 184 prophages (from 134 strains) were analyzed in more detail. Prophages were classified by comparing of specific structural proteins to those of previously classified phages using BLASTp. Among the prophages possible to classify, all belonged to the Caudovirales order, with higher prevalence of Siphoviridae (39.67%), followed by Myoviridae (19.57%) and Podoviridae (8.7%) families. The prophages sequences were aligned using MAFFT, and a distance matrix and a phylogenetic tree were constructed to evaluate similarities. A high diversity was found among the prophages, which may contribute to the diversity of *A. baumannii*, since some strains differ only on the integrated prophages. Furthermore, numerous potential virulence factors encoded by the prophages were detected, implicated in *A. baumannii* pathogenicity, namely antibiotic resistance, toxins, host interaction, survival and fitness.

Overall, our results demonstrate a high prevalence of prophages in *A. baumannii*. The amount and diversity of potential virulence factors encoded by the identified prophages point towards a significant contribution of these mobile elements for the dissemination and evolution of pathogenicity in this bacterial species.



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